



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Jeffrey M. Friedman, Yiyang Zhang, Ricardo Proenca, Margherita Maffei, Jeffrey Halaas, Ketan Gajiwala, and Stephen K. Burley
- (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
- (iii) NUMBER OF SEQUENCES: 99
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Klauber & Jackson
 - (B) STREET: 411 Hackensack Avenue
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/485,943
 - (B) FILING DATE: June 7, 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/438,431
 - (B) FILING DATE: May 10, 1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/347,563
 - (B) FILING DATE: November 30, 1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/292,345
 - (B) FILING DATE: August 17, 1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201 487-5800
 - (B) TELEFAX: 201 343-1684

a'
Sub B1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Jeffrey M. Friedman, Yiyang Zhang, Ricardo Proenca, Margherita Maffei, Jeffrey Halaas, Ketan Gajiwala, and Stephen K. Burley
- (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
- (iii) NUMBER OF SEQUENCES: 99
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Klauber & Jackson
(B) STREET: 411 Hackensack Avenue
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/485,943
(B) FILING DATE: June 7, 1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/438,431
(B) FILING DATE: May 10, 1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/347,563
(B) FILING DATE: November 30, 1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/292,345
(B) FILING DATE: August 17, 1994
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201 487-5800
(B) TELEFAX: 201 343-1684

a
Cont.
Sub
B1

(C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: Murine ob cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 57..560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA 56

ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG 104
Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
1 5 10 15

TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA 152
Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30

ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG 200
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45

CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT 248
Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
50 55 60

GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA 296
Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
65 70 75 80

GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG 344
Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
85 90 95

a' cont.
Sub B/

ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC	392
Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala	
100 105 110	
TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA	440
Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro	
115 120 125	
GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG	488
Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val	
130 135 140	
GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG	536
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln	
145 150 155 160	
TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA	588
Leu Asp Val Ser Pro Glu Cys *	
165	
ATCATGTAGA GGGAAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC	648
ACACATCCAT CATTCATTTTCTCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA	708
CAATGCTTGA CTCAAGTTAT CCACACAACCT TCATGAGCAC AAGGAGGGGC CAGCCTGCAG	768
AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG	828
TCCCACCTGC TCCGGGTACA TGTTCTCTCCG TGGGTACACG CTTGCTGCG GCCCAGGAGA	888
GGTGAGGTAG GGATGGGTAG AGCCTTTGGG CTGTCTCAGA GTCTTTGGGA GCACCGTGAA	948
GGCTGCATCC ACACACAGCT GGAACTCCG AAGCAGCACA CGATGGAAGC ACTTATTTAT	1008
TTATTCTGCA TTCTATTTTG GATGGATCTG AAGCAAGGCA TCAGCTTTTT CAGGCTTTGG	1068
GGGTCAGCCA GGATGAGGAA GGCTCCTGGG GTGCTGCTTT CAATCCTATT GATGGGTCTG	1128
CCCGAGGCAA ACCTAATTTT TGAGTACTG GAAGGAAGGT TGGGATCTTC CAAACAAGAG	1188
TCTATGCAGG TAGCGCTCAA GATTGACCTC TGGTGACTGG TTTTGTCTTCT ATTGTGACTG	1248
ACTCTATCCA AACACGTTTG CAGCGGCATT GCCGGGAGCA TAGGCTAGGT TATTATCAAA	1308
AGCAGATGAA TTTTGTCAAG TGTAATATGT ATCTATGTGC ACCTGAGGGT AGAGGATGTG	1368
TTAGAGGGAG GGTGAAGGAT CCGGAAGTGT TCTCTGAATT ACATATGTGT GGTAGGCTTT	1428
TCTGAAAGGG TGAGGCATTT TCTTACCTCT GTGGCCACAT AGTGTGGCTT TGTGAAAAGG	1488
ACAAAGGAGT TGAATCTTTT CGGAACATTT GGAGTGATACC AGGCACCTT GGAGGGGCTA	1548
AAGCTACAGG CCTTTTGTGTTG GCATATTGCT GAGCTCAGGG AGTGAGGGCC CCACATTGA	1608

21
Cont.

Sub
B1

GACAGTGAGC CCCAAGAAAA GGGTCCCTGG TGTAGATCTC CAAGGTTGTC CAGGTTGAT 1668
 CTCACAATGC GTTCTCTTAAG CAGGTAGACG TTTGCATGCC AATATGTGGT TCTCATCTGA 1728
 TTGGTTTCATC CAAAGTAGAA CCCTGTCTCC CACCCATTCT GTGGGGAGTT TTGTTCCAGT 1788
 GGGAAATGAGA AATCACTTAG CAGATGGTCC TGAGCCCTGG GCCAGCACTG CTGAGGAAGT 1848
 GCCAGGGCCC CAGGCCAGGC TGCCAGAATT GCCCTTCGGG CTGGAGGATG AACAAAGGGG 1908
 CTTGGGTTTT TCCATCACCC CTGCACCCTA TGTCACCATC AAAGTGGGGG GCAGATCAGT 1968
 GAGAGGACAC TTGATGGAAA GCAATACACT TTAAGACTGA GCACAGTTTC GTGCTCAGCT 2028
 CTGTCTGGTG CTGTGAGCTA GAGAAGCTCA CCACATACAT ATAAAAATCA GAGGCTCATG 2088
 TCCCTGTGGT TAGACCCTAC TCGCGGCGGT GTACTCCACC ACAGCAGCAC CGCACCGCTG 2148
 GAAGTACAGT GCTGTCTTCA ACAGGTGTGA AAGAACCTGA GCTGAGGGTG ACAGTGCCCA 2208
 GGGGAACCCT GCTTGCAGTC TATTGCATTT ACATACCGCA TTTCAGGGCA CATTAGCATC 2268
 CACTCCTATG GTAGCACACT GTTGACAATA GGACAAGGGA TAGGGGTTGA CTATCCCTTA 2328
 TCCAAAATGC TTGGGACTAG AAGAGTTTTG GATTTTAGAG TCTTTTCAGG CATAGGTATA 2388
 TTTGAGTATA TATAAAATGA GATATCTTGG GGATGGGGCC CAAGTATAAA CATGAAGTTC 2448
 ATTTATATTT CATAATACCG TATAGACACT GCTTGAAGTG TAGTTTTATA CAGTGTTTTA 2508
 AATAACGTTG TATGCATGAA AGACGTTTTT ACAGCATGAA CCTGTCTACT CATGCCAGCA 2568
 CTCAAAAACC TTGGGGTTTT GGAGCAGTTT GGATCTTGGG TTTTCTGTTA AGAGATGGTT 2628
 AGCTTATACC TAAAACCATA ATGGCAAACA GGCTGCAGGA CCAGACTGGA TCCTCAGCCC 2688
 TGAAGTGTGC CCTTCAGCC AGGTCATACC CTGTGGAGGT GAGCGGGATC AGGTTTTGTG 2748
 GTGCTAAGAG AGGAGTTGGA GGTAGATTTT GGAGGATCTG AGGGC 2793

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu

a'
 cont.
 Sub
 B1

1	5	10	15
Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys	20	25	30
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr	35	40	45
Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro	50	55	60
Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala	65	70	75
Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln	85	90	95
Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala	100	105	110
Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro	115	120	125
Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val	130	135	140
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln	145	150	155
Leu Asp Val Ser Pro Glu Cys *	165		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..546

a'
Cont.

Sub
B1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NNNGNNGTTG CAAGGCCCAA GAAGCCCANN NTCCTGGGAA GGAAA ATG CAT TGG 54
Met His Trp
1

GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC 102
Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val
5 10 15

CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC 150
Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile
20 25 30 35

AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC 198
Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val
40 45 50

TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC 246
Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His
55 60 65

CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA 294
Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln
70 75 80

CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC 342
Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn
85 90 95

GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG 390
Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys
100 105 110 115

AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC CTG 438
Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu
120 125 130

GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC CTG 486
Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu
135 140 145

AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC 534
Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu
150 155 160

AGC CCT GGG TGC TGAGGCCTT GAAGGTCACCT CTCCTGCAA GGACTNACGT 585
Ser Pro Gly Cys
165

TAAGGGAAGG AACTCTGTTT TCCAGGTATC TCCAGGATTG AAGAGCATTG CATGGACACC 645

CCTTATCCAG GACTCTGTCA ATTTCCCTGA CTCCTCTAAG CCACTCTTCC AAAGG 700

A'
Cont.

Sub
B1

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Human ob polypeptide

(vi) ORIGINAL SOURCE: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
1 5 10 15
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45
Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
50 55 60
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
65 70 75 80
Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
85 90 95
Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
100 105 110
Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
115 120 125
Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
130 135 140
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
145 150 155 160
Leu Asp Leu Ser Pro Gly Cys
165

(2) INFORMATION FOR SEQ ID NO:5:

a1
Cont.
Sub
B1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide lacking Gln at position 49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
1 5 10 15
Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45
Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly
50 55 60
Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val
65 70 75 80
Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile
85 90 95
Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe
100 105 110
Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu
115 120 125
Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
130 135 140
Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu
145 150 155 160
Asp Val Ser Pro Glu Cys
165

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Q1
Cont.
Sub
B1

(ii) MOLECULE TYPE: protein

(A) Description: Human ob polypeptide lacking Gln at position 49

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
1 5 10 15
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45
Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly
50 55 60
Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val
65 70 75 80
Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile
85 90 95
Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe
100 105 110
Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp
115 120 125
Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val
130 135 140
Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu
145 150 155 160
Asp Leu Ser Pro Gly Cys
165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: exon 2G7

(iii) HYPOTHETICAL: NO

a!
cont.
Sub
B1

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG TGTOGGGTCC 60
NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC TATCCAGAAA GTCCAGGATG 120
ACACCAAAAG CCTCATCAAG ACCATTGTCA NCAGGATCAC TGANATTTCA CACACG 175

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) PCR 5' primer for exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCAGGGCAGG AAAATGTG 18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) PCR 3' primer for exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATCCTGGAC TTTCTGGATA GG 22

(2) INFORMATION FOR SEQ ID NO:10:

a' Cont.
Sub B1

- a' cont.
Sub B1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA 60
TTCCCCTCTA CAAATAATTT TGTTTAACTT TAAGAAGGAG ATATACC ATG GGC AGC 116
Met Gly Ser
1
AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG CGC GGC AGC 164
Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
5 10 15
CAT ATG CTC GAG GAT CCC GCT GCT AAC AAA GCC CGA AAG GAA GCT GAG 212
His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys Glu Ala Glu
20 25 30 35
TTG GCT GCT GCC ACC GCT GAG CAA TAA CTA G CATAACCCCT TGGGGCCTCT 263
Leu Ala Ala Ala Thr Ala Glu Gln *
40
AAACGGGTCT TGAGGGGTTT TTTG 287

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15
Arg Gly Ser His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys
20 25 30
Glu Ala Glu Leu Ala Ala Ala Thr Ala Glu Gln
35 40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Murine 5' primer

a!
cont.
Sub B1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTATGTTCA TATGGTGCCG ATCCAGAAAG TC

32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Murine 3' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCCCTCTACA TATGTCTTGG GAGCCTGGTG GC

32

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Human 5' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTATGTCCA TATGGTGCCG ATCCAAAAAG TC

32

a' cont.
Sub B1

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Human 3' primer
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: Yes
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
TTCCTTCCCA TATGGTACTC CTTGCAGGAA GA

32

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - (A) DESCRIPTION: Splice acceptor site in ob
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: Splice acceptor site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
AGCAGTCGGT A

11

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

a!
cont.
Sub
B1

(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr	Leu	Ile	Lys	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu	His	Pro	Ile	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu

a!
cont.
Sub
B1

1 5 10 15

Ser Leu Asp

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
 - (A) DESCRIPTION: ob peptide fragment
- (v) FRAGMENT TYPE: Carboxyl terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val
1 5 10 15

Ser Pro Glu Cys
20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
 - (A) DESCRIPTION: portion of the human ob gene including noncoding sequence upstream of first exon, coding sequence of first exon, and 5' region of first intron
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 38..181
- (ix) FEATURE:

a' Cont.
Sub B1

(A) NAME/KEY: 5' region of first intron
(B) LOCATION: 182..414

(ix) FEATURE:

(A) NAME/KEY: 5' noncoding sequence of the human ob gene from which the HOB 1gF DNA primer was generated
(B) LOCATION: 11..28

(ix) FEATURE:

(A) NAME/KEY: intronic sequence of the human ob gene from which the HOB 1gR primer was generated
(B) LOCATION: 241..260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTTGCAAGG	CCCAAGAAGC	CCATCCTGGG	AAGGAAA	ATG	CAT	TGG	GGA	ACC	CTG	55
				Met	His	Trp	Gly	Thr	Leu	
				1				5		
TGC	GGA	TTC	TTG	TGG	CTT	TGG	CCC	TAT	CTT	103
Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	Leu	
			10				15			
									20	
CCC	ATC	CAA	AAA	GTC	CAA	GAT	GAC	ACC	AAA	151
Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	
			25				30			
									35	
GTC	ACC	AGG	ATC	AAT	GAC	ATT	TCA	CAC	ACG	201
Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	
			40						45	
CAAAGTAGAA	CTGCAGCCAG	CCCAGCACTG	GTCCTAGTG	GCACTGGACC	CAGATAGTCC	261				
AAGAAACATT	TATTGAACGC	CTCCTGAATG	CCAGGCACCT	ACTGGAAGCT	GAGAAGGATT	321				
TTGGATAGCA	CAGGGCTCCA	CTCTTCTG	TTGTTTCTTN	TGGCCCCCTC	TGCCTGCTGA	381				
GATNCCAGGG	GTTAGNGGTT	CTTAATTCT	AAA			414				

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: N-terminal portion of the human ob protein encoded by first exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

a' cont.
Sub B, 7

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
 1 5 10 15
 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
 - (A) DESCRIPTION: portion of the human ob gene including 3' region of first intron, coding sequence of second exon, and 3' noncoding sequence
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 291..648
- (ix) FEATURE:
 - (A) NAME/KEY: 3' of first intron
 - (B) LOCATION: 1..290
- (ix) FEATURE:
 - (A) NAME/KEY: intronic sequence of the human ob gene HOB from which the HOB 2gF primer was generated
 - (B) LOCATION: 250..269
- (ix) FEATURE:
 - (A) NAME/KEY: 3' noncoding sequence of the human ob gene from which the HOB 2gR DNA primer was generated
 - (B) LOCATION: 707..728
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGGTTCTTT CAGGAAGAGG CCATGTAAGA GAAAGGAATT GACCTAGGGA AAATTGGCCT 60
 GGGAAGTGGA GGGAACGGAT GGTGTGGGAA AAGCAGGAAT CTCGGAGACC AGCTTAGAGG 120
 CTTGGCAGTC ACCTGGGTGC AGGANACAAG GGCCTGAGCC AAAGTGGTGA GGGAGGGTGG 180

a!
 cont.
 sub
 B/

AAGGAGACAG CCCAGAGAAT GACCCTCCAT GCCCACGGGG AAGGCAGAGG GCTCTGAGAG 240
 CGATTCTCC CACATGCTGA GCACTTGTTT TCCCTCTTCC TCCTNCATAG CAG TCA 296
 Gln Ser
 1
 GTC TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC 344
 Val Ser Ser Lys Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu
 5 10 15
 CAC CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC 392
 His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr
 20 25 30
 CAA CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC 440
 Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser
 35 40 45 50
 AAC GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT 488
 Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser
 55 60 65
 AAG AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC 536
 Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser
 70 75 80
 CTG GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC 584
 Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala
 85 90 95
 CTG AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC 632
 Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp
 100 105 110
 CTC AGC CCT GGG TGC T GAGGCCTTGA AGGTCACTCT TCCTGCAAGG ACTACGTAA 688
 Leu Ser Pro Gly Cys
 115
 GGGAAGGAAC TCTGGCTTTC CAGGTATCTC CAGGATTGAA GAGCATTGCA TGGACACCCC 748
 TTATCCAGGA CTCTGTCAAT TTCCCTGACT CCTCTAAGCC ACTCTTCCAA AGG 801

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: C-terminal portion of the human ob protein encoded by second exon

a'
 cont.
 Sub
 B'

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
1 5 10 15
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
20 25 30
Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
35 40 45
Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
50 55 60
Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
65 70 75 80
Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
85 90 95
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
100 105 110
Leu Asp Leu Ser Pro Gly Cys
115

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Glu Lys Arg Glu Ala Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

a1
cont.
Sub
B1

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu Ala Glu Ala

1

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Glu Lys Arg

1

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: HOB 1gF DNA primer generated from the 5' noncoding sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCAAGAAGC CCATCCTG

18

(2) INFORMATION FOR SEQ ID NO:30:

Q1
Cont.
Sub
B1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: HOB 1gR DNA primer generated from the first intronic sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTATCTGG GTCCAGTGCC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: HOB 2gF DNA primer generated from the first intronic sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCACATGCTG AGCACTTGTT

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: HOB 2gR DNA primer generated from the 3' noncoding sequence of the human ob gene

a' cont.
Sub B1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTCAATCCT GGAGATACCT GG

22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA

(A) DESCRIPTION: pPIC.9 cloning site

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCGAGAAAA GAGAGGCTGA AGCTTACGTA GAATTCCTTA GGCCGGCCGG G

51

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) PCR 5' primer for amplifying human ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTATCTCTCG AGAAAAGAGT GCCCATCCAA AAAGTCCAAG

40

(2) INFORMATION FOR SEQ ID NO:35:

Q1
cont.
Sub
B1

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)
 (A) PCR 3' primer for amplifying human ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCGCGAATTC TCAGCACCCA GGGCTGAGGT C

31

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)
 (A) PCR 5' primer for amplifying murine ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTATCTCTCG AGAAAAGAGT GCCTATCCAG AAAGTCCAGG

40

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (primer)
 (A) PCR 3' primer for amplifying murine ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

a!
cont.
Sub
B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCGAATTC TCAGCATTCA GGGCTAACAT C

31

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: tetrapeptide at N-terminus of renatured murine ob protein after thrombin cleavage

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Ser His Met

1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS1734

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGACAAAT GAGATAAGG

19

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs

a1
cont.
Sub
B1

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS1734

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAGTTACAG CTTTACAG

18

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS494

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTAAACACCT TTCCATTCC

19

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS494

(iii) HYPOTHETICAL: NO

a1 cont.
Sub B1

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TTATATTCAC TTTTCCCCTC TC

22

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS883

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGCAGTAAGC TGTGATTGAG

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS883

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTGCAGCTTT AATTGTGAGC

20

at
cont.
Sub
B1

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AGTGTGTGTG TTCTCCTG

18

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2359
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAAGGGGATG TGATAAGTG

19

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)

a!
cont.
sub
B1

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS2336

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTGTTACGT TTAGTTAC

18

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS2336

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGAATAATGA GAGAAGATTG

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS1218

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

a
cont.
506
B1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTCAACTGA CAGAAAAC

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS1218

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GACTATGTAA AAGAAATGCC

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS1402

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AAAGGGCTTC TAATCTAC

18

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

*a1
cont.
sub
B1*

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS1402

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCTTCCAAC TCTTTGAC

18

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS999

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TAAACCCCT TTCTGTTC

18

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS999

(iii) HYPOTHETICAL: NO

a1 cont.
Sub B1

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTGCATAATA GTCACACCC

19

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1751

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCAAAATCAG AATTGTCAGA AG

22

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1751

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAACCGAAGT TCAGATACAG

20

a!
cont.

Sub
B1

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1174

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AATATCTGAC ATTGGCAC

18

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1174

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TTAGACCTGA GAAAAGAG

18

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

a!
cont.

sub
B1

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS2061

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GTTGCACAAT ACAAATCC

19

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS2061

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTTCCATTAG TGTCTTATAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS2588

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

a!
Cont.

Sub
B1

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCACTACAC ACCTAATC

18

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS2588

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCATTCTACA TTTCCACC

18

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS808

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GGCTGTGTGA GCAAGATCCT AGGA

24

(2) INFORMATION FOR SEQ ID NO:64:

a' Cent.
SUB B)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS808

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TTGCCAGGCA AAGAGGGCTG GAC

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1392

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTCAGGTATG TCTTTATC

18

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1392

a!
Cont.

Sub
B1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGTCTCTGCA TTCTTTTC

18

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1148

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GACACATACA AACACAAG

18

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS1148

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

a!
Cont.
Sub
B1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATTGAGTTGA GTGTAGTAG

19

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS1529

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGGGATTTC TAATTGTC

18

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS1529

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AAAAGATGGA GGCTTTTG

18

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

a!
Cont.
506
B1

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS2619

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGTTAAGGGA AGGAACTCTG G

21

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS2619

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGCTTAGAG GAGTCAGGGA

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer swSS404

(iii) HYPOTHETICAL: NO

a'
Cont.

Sub
B'

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCAGGGTCA ATACAAAG

18

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS404

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TAATGTGTCC TTCTTGCC

18

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: sequence tagged-site specific PCR primer SWSS2367

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAATCCTGGC TTCATTG

18

a!
Cont
Sub
B1

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: sequence tagged-site specific PCR primer sWSS2367
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGGTGGGTA GGATGCTA

18

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Marker UT528
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGCAGTAAGC TGTGATTGAG

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

a' cont,
SUB B1

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker UT528

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTGCAGCTTT AATTGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFMa065zg9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGCTTCAAGA CTTTNA GCCT

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFMa065zg9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

a!
Cont
Sub
B17

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGTCAGCAGC ACTGTGATT

19

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFMa125wh1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCACCTTGAG ATTCCATCC

19

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFMa125wh1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AACACCGTGG TCTTATCAAA

20

(2) INFORMATION FOR SEQ ID NO:83:

a'
cont.
s
B)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Marker AFM309yf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CATCCAAGTT GGCAGTTTTT

20

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Marker AFM309yf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AGATGCTGAA TTCCAGACA

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Marker AFM218xf10

a¹
Cont-

Sub
B-1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGGGCAACAC AGCAAA

16

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFM218xf10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCAGTTAGT GCCAATGTCA

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Marker AFM206xc1

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

at
cont
501
B1

CCAGGCCATG TGGAAC

16

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Marker AFM206xc1
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGTTCTTGGC TTGCGTCAGT

20

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (primer)
 - (A) DESCRIPTION: Marker AFM199xh12
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCTGATTGCT GGCTGC

16

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid

Q1
Cont.
sub
B1

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFM199xh12

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCGCGTGTGT ATGTGAG

17

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFMa345wc9

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTCTTGGC AAACACAT

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)
(A) DESCRIPTION: Marker AFMa345wc9

(iii) HYPOTHETICAL: NO

al
cont

sub
B1

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCCTAAGGGA ATGAGACACA

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: primer for mouse Pax4 gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGAGCCTTG TCCTGGGTAC AAAG

24

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) DESCRIPTION: Recombinant murine met ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: murine

(ix) FEATURE:

(A) NAME/KEY: CDS

a!
cont.
sub
B1

(B) LOCATION: 41..478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TCTAGATTG AGTTTAACT TTTAGAAGGA GGAATAACAT ATG GTA CCG ATC CAG 55
Met Val Pro Ile Gln
1 5

AAA GTT CAG GAC GAC ACC AAA ACC TTA ATT AAA ACG ATC GTT ACG CGT 103
Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg
10 15 20

ATC AAC GAC ATC AGT CAC ACC CAG TCG GTC TCC GCT AAA CAG CGT GTT 151
Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ala Lys Gln Arg Val
25 30 35

ACC GGT CTG GAC TTC ATC CCG GGT CTG CAC CCG ATC CTA AGC TTG TCC 199
Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser
40 45 50

AAA ATG GAC CAG ACC CTG GCT GTA TAC CAG CAG GTG TTA ACC TCC CTG 247
Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu
55 60 65

CCG TCC CAG AAC GTT CTT CAG ATC GCT AAC GAC CTC GAG AAC CTT CGC 295
Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg
70 75 80 85

GAC CTG CTG CAC CTG CTG GCA TTC TCC AAA TCC TGC TCC CTG CCG CAG 343
Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln
90 95 100

ACC TCA GGT CTT CAG AAA CCG GAA TCC CTG GAC GGG GTC CTG GAA GCA 391
Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu Ala
105 110 115

TCC CTG TAC AGC ACC GAA GTT GTT GGT CTG TCC CGT CTG CAG GGT TCC 439
Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser
120 125 130

CTT CAG GAC ATC CTT CAG CAG CTG GAC GTT TCT CCG GAA TGT TAATGGA 488
Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu Cys
135 140 145

TCC 491

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: Recombinant murine met ob protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
1 5 10 15
Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
20 25 30
Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
35 40 45
Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
50 55 60
Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp
65 70 75 80
Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser
85 90 95
Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
100 105 110
Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
115 120 125
Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser
130 135 140
Pro Glu Cys
145

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 454 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(A) DESCRIPTION: Recombinant human met ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

a'
cont
sub
B1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAT ATG GTA CCG ATC CAG AAA GTT CAG GAC GAC ACC AAA ACC TTA ATT 48
Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile
1 5 10 15

AAA ACG ATC GTT ACG CGT ATC AAC GAC ATC AGT CAC ACC CAG TCG GTG 96
Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val
20 25 30

AGC TCT AAA CAG CGT GTT ACA GGC CTG GAC TTC ATC CCG GGT CTG CAC 144
Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His
35 40 45

CCG ATC CTG ACC TTG TCC AAA ATG GAC CAG ACC CTG GCT GTA TAC CAG 192
Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln
50 55 60

CAG ATC TTA ACC TCC ATG CCG TCC CGT AAC GTT CTT CAG ATC TCT AAC 240
Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn
65 70 75

GAC CTC GAG AAC CTT CGC GAC CTG CTG CAC GTG CTG GCA TTC TCC AAA 288
Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys
80 85 90 95

TCC TGC CAC CTG CCA TGG GCT TCA GGT CTT GAG ACT CTG GAC TCT CTG 336
Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu
100 105 110

GGC GGG GTC CTG GAA GCA TCC GGT TAC AGC ACC GAA GTT GTT GCT CTG 384
Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu
115 120 125

TCC CGT CTG CAG GGT TCC CTT CAG GAC ATG CTT TGG CAG CTG GAC CTG 432
Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu
130 135 140

TCT CCG GGT TGT TAATGGATCC 454
Ser Pro Gly Cys
145

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

a!
cont
svb
B1

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: Recombinant human met ob protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
1 5 10 15
Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
20 25 30
Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
35 40 45
Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
50 55 60
Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
65 70 75 80
Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
85 90 95
Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
100 105 110
Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
115 120 125
Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
130 135 140
Pro Gly Cys
145

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15
Arg Gly Ser His Met

a1
Cont-
Sub
B1

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser Pro
20

Q1
cont
Sub
BI